Fingerprinting Analysis of the Introgressed lines from *Gossypium hirsutum* L. × *G. barbadense* L. based on AFLP markers

LIU Zhao-hui[1], ZHANG Yong[2], DONG Shun-wen[1], WANG Jun[1]

(1. *Industrial Crop Breeding and Cultivation Institute, Sichuan Academy of Agriculture Sciences, Jianyang, Sichuan* 641400, *China*; 2. *School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu, Sichuan* 610054, *China*)

The main cultivated varieties in the world belong to the species of upland cotton (*Gossypium hirsutum* L.), and their genetic background is very narrow. However, the wild species and races in the genus of *Gossypium* have abundant genetic diversity and possess lots of excellent genes with potential high yield, fine and strong fiber, disease and insect resistance, drought and coldness resistance, male sterility, and so on. The interspecific hybridization for utilizing the beneficial genes from these wild tetraploid species had been widely carried out for 20 years in China. It has huge practical and theoretical value to conduct the analyses of the cotton introgression lines of interspecific hybridization toward upland cotton, which helped to successfully develop the introgressed lines resistant to the carmine spider mite (*Tetranychus cinnabarinus*) and to the cotton aphid (*Aphis gossypii*) in Sichuan. In this paper, the genetic background and phylogeny of 9 introgression lines from same interspecific hybridization of *G. hirsutum* × *G. barbadense* L. and 2 relative lines based on AFLP analysis. The results indicated that AFLP was an efficient technique to distinguish the different cultivars by their unique AFLP fingerprint patterns. Further more, some unique AFLP markers were detected for 9 cotton lines, which could be used to develop specific probes for identification purposes. Based on 16 pairs of AFLP primers, 672 bands altogether were amplified, and the percent of polymorphic bands was 91.2%. Average paired similarity coefficient among germplasm was 0.6147, ranged from 0.4641. The AFLP cluster dendrogram of 11 lines of cotton was constructed with 3 groups: TM-1, the cotton lines resistant to red spider, and the lines resistant to aphid. The result of AFLP cluster analysis fitted basically with that of their pedigrees and morphological traits.

Key words: introgressed line; tetraploid; molecular phylogeny; fingerprinting; AFLP